601-1-077

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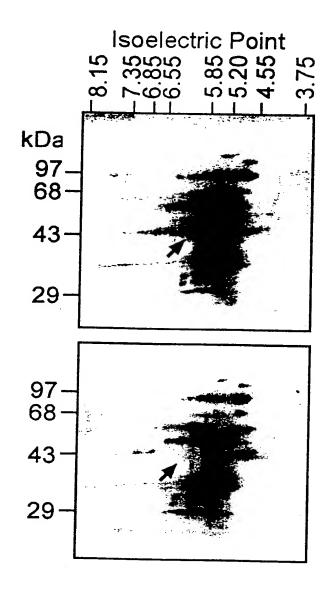


Figure 1

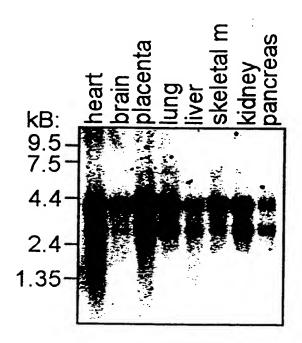


Figure 2

Fig.2

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~	1 COCOGNAGOCAGANTOGOACTECAAGCETACCTECTEAGGGGGGGGGGGGAAGGGGAAGGGAA
	A P A A I L M O A M A M A B A B A B V B I I I V A I I I I O M A M A B A B A B A B V B I I I I I I I I I I I I I I I I I
121	121 TOTCCCTGGGCCGTGCGGACCCTGAGGAAGAGCTCACCTTTGCCCTGAGACAGCAAATGTGGAAACTCTCGGAGCTGGAGCTGGAGCTGGAATCCCAGCTCTCCTAAT 8 L G R A D P E E E L 8 L T F A L R Q Q N V E R L 8 E L V Q A V 8 D P 8 S P Q Y
241	1 ACGGAAAATAGCTGAGCCCTAGAAATGTGGTGATGTGAGGCCATGCACTGCACACAGTGGAAAAATGGCTCTTGGGAGCCGAAAGTGCCATTCTGTGATCA G K Y L T L E N V A D L V R P S P L T L H T V Q K W L L A A G A G K C H B V I T
361	L CACAGGACTITCTGACTTGCTGACATCCGACAAGCTGCTGCTGCTGAGTTTCATCACTATGTGGGAGGACGACCCAACGGAAACCCAAGATATTGTAAGATCCCACAAC O D F L T C W L S I R Q A E L L L P G A B F H H Y V G G P T E T H V V R S P H P
481	1 CCTACCAGCTTCCACAGGCCTTGGCCCCCCATGTGGGGAACTGCACCATTTTCCCCCAACATCATCCCTGAGGCAACGTGTGAGGCAAGGAGTGAGAGGAACTGTAAGGC Y Q L P Q A L A P H V D F V G G L H I F P P T S S L R Q R P K P Q V T G T V U <sub>A</sub> ll
109	THCATCINGGGGGAAACCCCTCTGTAAACGAATACAACTTGACCTCACAAAAACAAGAAAAACAACAAAACCTGTGCCAATTCCTGGAGCAGTTTCCTTGAAAAACAGAAACCTGTGAAAAAAAA
721	** I ATGACTCADACCTOGGCTCAGTTCATGCGCACTTTGCACATCAGGCATCAGTAGCCCGTGTGGATTGGACACAGGGCCGGGGCCGGGACTTGAGGCCAGTCTAG  D S D L A Q F H R L F G G N F A H Q A S V A R V V G Q Q G R G R A G I E A S L D
841	I ATGTGCAGTACCTGATGCTGCTGCCAACATCCTCCACCTGGGTCTACAGTAGCCCTGGCGATGGAAGCCCTTCCTGCAGTGGCTCATGCTGCTGCTCAGTAATGAGTCAG V Q Y L M S A G A NILS T W V Y S S P O R H E U O K P F L G W L M L L S N E S A
196	L CCCTGCCACATGCTGATACTGTGATGGATGATGATGGATG
081	TCGCCTCAGGTGACAGTGGGTGTTGGTCTGTCTCTGGAAGACACCAGTTCCGCCTTCCTGCCTCCAGCCCTATGTCACAGTGGGAGGCACATCCTTCCAGGAAC A 8 G D S G A G C W S V S G R H Q F R P T F P A 8 8 P Y V T T V G G T S F Q B P
201	I CTITCCTCATCACAAATGATAAATAATAATAATGAGGAGGAGGAGGAAATGAGGAATGCTCAAGAGAAAGAA
321	1 TOCCACCATCCAGTTACTTCAATGCCAGTGCCTACCCAGATGTGGCTGCACTTTCTGATGGCTACTGGGGTGGTCACAGAGAGGCCATTCCATGGGTGTCCAGGAACCTCGG
441	1 CCTCTACTCCAGTGTTTOGGGGGATCCTATACCATAGAGCACAGAATCCTTAGTGGCCGCCCCCTCTTGGCTTTCTCAACGCTCTACCAGGAGCATGGAGGACTCT S T P V P G G I L S L I N E H R I L S G R P P L G P L N P R L Y Q G H G A G L P
195	TTGATGTAACCCGTGGCTGCCATGAGCTGTCTGGAAAAAGGGAAGAAGGGCCAGGGTTTCTGCTCTGGTGGCTGGGAAACAGGCTGGGGAACACCCCAACTTCCCAAGTT   D V T R G C H E 8 C L D E E V E G Q G P C S G P G W D P V T G W G T P N P P A L
681	1 TOCTGAAGACTCTAACCCCTGACCCTTTCCTATCAGGAGAAGATGGCTTGTCCCCTGAAGCTGGCAGTTCAGTCCCTTATTCTGCCCTGTTGGAAGCCCTGCTGAACCCTCA L K T L L N P .
921	ACTATTOACTGCAGACAGCCTAATCCCCTGAAATGCTGTGAGCTTGACTTGACTTCCAACCCTACCATCATCAGTCTCCATGCTCCAGGTCTCCCTACTCCTGCTTGCT
2521 2521 2641 2761 2881 3001 3121 3241	1 TUTAAGNTGCUTGATACCAACATTECATCGTCCACCECAAACCAAATTECATTCTTGTTTGTTAAATGATGCTATGCT

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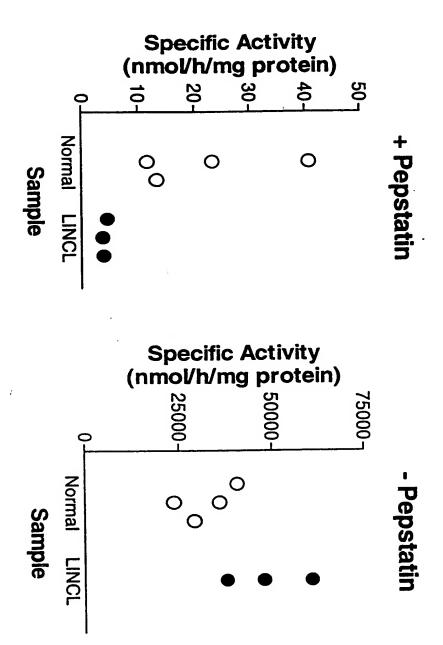


Figure 5